==========

Sequence Listing could not be accepted.
If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2008; month=1; day=24; hr=14; min=16; sec=47; ms=367;]

==========

****

Reviewer Comments:
<210> 4
<211> 25
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: GRK6 peptide sequence

<400> 4

Leu	Leu	Gln	Arg	Leu	Phe	Ser	Arg	Gln	Asp	Cys	Cys	Gly	Asn	Cys	Ser
1				5				10						15	

Asp	Ser	Glu	Glu	Glu	Leu	Pro	Thr	Arg
		20				25		

The above <213> response is invalid, per Sequence Rules. The only valid responses are: the Genus species of the organism, "Artificial Sequence," or "Unknown." (do not add "Organism" to it). This error appears in subsequent sequences, too.

****

Validated By CRFValidator v 1.0.3

Application No: 10588114 Version No: 1.0

Input Set:

Output Set:

Started: 2008-01-14 17:30:10.651
Finished: 2008-01-14 17:30:18.512
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 861 ms
Total Warnings: 67
Total Errors: 0
No. of SeqIDs Defined: 99
Actual SeqID Count: 99

Error code		Error Description
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W	402	Undefined organism found in <213> in SEQ ID (4)
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W	402	Undefined organism found in <213> in SEQ ID (17)
W	402	Undefined organism found in <213> in SEQ ID (19)
W	402	Undefined organism found in <213> in SEQ ID (23)
W	213	Artificial or Unknown found in <213> in SEQ ID (24)
W	213	Artificial or Unknown found in <213> in SEQ ID (25)
W	213	Artificial or Unknown found in <213> in SEQ ID (26)
W	213	Artificial or Unknown found in <213> in SEQ ID (27)
W	213	Artificial or Unknown found in <213> in SEQ ID (28)
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W	213	Artificial or Unknown found in <213> in SEQ ID (31)
W	213	Artificial or Unknown found in <213> in SEQ ID (32)
W	213	Artificial or Unknown found in <213> in SEQ ID (33)
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Input Set:

Output Set:

Started: 2008-01-14 17:30:10.651
Finished: 2008-01-14 17:30:18.512
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 861 ms
Total Warnings: 67
Total Errors: 0
No. of SeqIDs Defined: 99
Actual SeqID Count: 99

Error code		Error Description
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W	213	Artificial or Unknown found in <213> in SEQ ID (59)
W	213	Artificial or Unknown found in <213> in SEQ ID (60)

This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING

<110> OSTERMEIER, MARC A.
GUNTAS, GURKAN

<120> METHODS FOR MAKING AND USING MOLECULAR SWITCHES
INVOLVING CIRCULAR PERMUTATION

<130> 71699/62568

<140> 10588114
<141> 2008-01-14

<150> PCT/US05/002633
<151> 2005-01-28

<150> 60/628,997
<151> 2004-11-18

<150> 60/607,684
<151> 2004-09-07

<150> 60/557,152
<151> 2004-03-26

<150> 60/539,774
<151> 2004-01-28

<160> 99

<170> PatentIn Ver. 3.3

<210> 1
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide linker

<400> 1
Gly Ser Gly Gly Gly
1 5

<210> 2
<211> 37
<212> PRT
<213> Homo sapiens

<400> 2
Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser
1 5 10 15

Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr

20 25 30

Met Gly Leu Leu Thr
35

<210> 3
<211> 14
<212> PRT
<213> Rous sarcoma virus

<400> 3
Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg
1 5 10

<210> 4
<211> 25
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: GRK6 peptide sequence

<400> 4
Leu Leu Gln Arg Leu Phe Ser Arg Gln Asp Cys Cys Gly Asn Cys Ser
1 5 10 15

Asp Ser Glu Glu Glu Leu Pro Thr Arg
20 25

<210> 5
<211> 7
<212> PRT
<213> Monkey virus SV40

<400> 5
Pro Lys Lys Lys Lys Lys Val
1 5

<210> 6
<211> 6
<212> PRT
<213> Homo sapiens

<400> 6
Ala Arg Arg Arg Arg Pro
1 5

<210> 7
<211> 10
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: NF kappa-B p50
sequence

<400> 7
Glu Glu Val Gln Arg Lys Arg Gln Lys Leu
1 5 10

<210> 8
<211> 9
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: NF kappa-B p65
sequence

<400> 8
Glu Glu Lys Arg Lys Arg Thr Tyr Glu
1 5

<210> 9
<211> 21
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Nucleoplasmin
sequence

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1 5 10 15

Lys Lys Lys Leu Asp
20

<210> 10
<211> 5
<212> PRT
<213> Homo sapiens

<400> 10
Lys Phe Glu Arg Gln
1 5

<210> 11
<211> 36
<212> PRT
<213> Homo sapiens

<400> 11

Met Leu Ile Pro Ile Ala Gly Phe Phe Ala Leu Ala Gly Leu Val Leu
1 5 10 15

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20 25 30

Tyr Gln Thr Ile
35

<210> 12
<211> 35
<212> PRT
<213> Homo sapiens

<400> 12
Leu Val Pro Ile Ala Val Gly Ala Ala Leu Ala Gly Val Leu Ile Leu
1 5 10 15

Val Leu Leu Ala Tyr Phe Ile Gly Leu Lys His His His Ala Gly Tyr
20 25 30

Glu Gln Phe
35

<210> 13
<211> 27
<212> PRT
<213> Saccharomyces cerevisiae

<400> 13
Met Leu Arg Thr Ser Ser Leu Phe Thr Arg Arg Val Gln Pro Ser Leu
1 5 10 15

Phe Ser Arg Asn Ile Leu Arg Leu Gln Ser Thr
20 25

<210> 14
<211> 25
<212> PRT
<213> Saccharomyces cerevisiae

<400> 14
Met Leu Ser Leu Arg Gln Ser Ile Arg Phe Phe Lys Pro Ala Thr Arg
1 5 10 15

Thr Leu Cys Ser Ser Arg Tyr Leu Leu
20 25

<210> 15
<211> 64
<212> PRT
<213> Saccharomyces cerevisiae

<400> 15
Met Phe Ser Met Leu Ser Lys Arg Trp Ala Gln Arg Thr Leu Ser Lys
1 5 10 15

Ser Phe Tyr Ser Thr Ala Thr Gly Ala Ala Ser Lys Ser Gly Lys Leu
20 25 30

Thr Gln Lys Leu Val Thr Ala Gly Val Ala Ala Ala Gly Ile Thr Ala
35 40 45

Ser Thr Leu Leu Tyr Ala Asp Ser Leu Thr Ala Glu Ala Met Thr Ala
50 55 60

<210> 16
<211> 41
<212> PRT
<213> Saccharomyces cerevisiae

<400> 16
Met Lys Ser Phe Ile Thr Arg Asn Lys Thr Ala Ile Leu Ala Thr Val
1 5 10 15

Ala Ala Thr Gly Thr Ala Ile Gly Ala Tyr Tyr Tyr Tyr Asn Gln Leu
20 25 30

Gln Gln Gln Gln Gln Arg Gly Lys Lys
35 40

<210> 17
<211> 4
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Endoplasmic
reticulum localizing sequence

<400> 17
Lys Asp Glu Leu
1

<210> 18
<211> 15
<212> PRT
<213> Human adenovirus type 19

<400> 18
Leu Tyr Leu Ser Arg Arg Ser Phe Ile Asp Glu Lys Lys Met Pro
1 5 10 15

<210> 19
<211> 20
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Interleukin-2
sequence

<400> 19
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1 5 10 15

Val Thr Asn Ser
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<210> 20
<211> 29
<212> PRT
<213> Homo sapiens

<400> 20
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr
20 25

<210> 21
<211> 27
<212> PRT
<213> Homo sapiens

<400> 21
Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1 5 10 15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn
20 25

<210> 22
<211> 18
<212> PRT
<213> Influenza A virus

<400> 22
Met Lys Ala Lys Leu Leu Val Leu Leu Tyr Ala Phe Val Ala Gly Asp
1 5 10 15

Gln Ile

<210> 23

<211> 24
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Interleukin-4
sequence

<400> 23
Met Gly Leu Thr Ser Gln Leu Leu Pro Pro Leu Phe Phe Leu Leu Ala
1 5 10 15

Cys Ala Gly Asn Phe Val His Gly
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<210> 24
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 24
tgccggatcc ggcggtggcc acccagaaac gctggtg 37

<210> 25
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 25
gtctgaggat ccccaatgct taatcagtga 30

<210> 26
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 26
gccgttaatc cagattac 18

<210> 27
<211> 41

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<220>
<221> modified_base
<222> (18)..(19)
<223> a, c, g, t, unknown, or other

<220>
<221> modified_base
<222> (21)..(22)
<223> a, c, g, t, unknown, or other

<400> 27
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<210> 28
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 28
gaagataatg tcagggcc 18

<210> 29
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<220>
<221> modified_base
<222> (19)..(20)
<223> a, c, g, t, unknown, or other

<400> 29
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<210> 30
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 30
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<210> 31
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

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<221> modified_base
<222> (19)..(20)
<223> a, c, g, t, unknown, or other

<400> 31
gcttacccga tcgctgttnn kgcgttatcg ctgatttat 39

<210> 32
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 32
cgggccgttg atggtcat 18

<210> 33
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<220>
<221> modified_base
<222> (19)..(20)
<223> a, c, g, t, unknown, or other

<400> 33
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<210> 34
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 34
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<210> 35
<211> 1995
<212> DNA
<213> Escherichia coli

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tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggctg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttacccga tcgctgttga agcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
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cccgaagaac gttttccaat gatgagcact tttaaagttc tgctatgtgg cgcggtatta 1560
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cgtatcacca agtaa 1995

<210> 36
<211> 664

<212> PRT
<213> Escherichia coli

<400> 36

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Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
            20                  25                  30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
        35                  40                  45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
    50                  55                  60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
65                  70                  75                  80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
                85                  90                  95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
            100                 105                 110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
        115                 120                 125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
    130                 135                 140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
145                 150                 155                 160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
                165                 170                 175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
            180                 185                 190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
        195                 200                 205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
    210                 215                 220

Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
225                 230                 235                 240

Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
                245                 250                 255

Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
            260                 265                 270

Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
        275                 280                 285
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Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
    290                 295                 300

Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
305                 310                 315                 320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
                325                 330                 335

Leu Ala Lys Asp Pro Arg Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp
            340                 345                 350

Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr
        355                 360                 365

Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met
    370                 375                 380

Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala
385                 390                 395                 400

Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg
                405                 410                 415

Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val
            420                 425                 430

Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg
        435                 440                 445

Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser
    450                 455                 460

His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
465                 470                 475                 480

Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
                485                 490                 495

Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
            500                 505                 510

Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu
        515                 520                 525

Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
    530
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